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## RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/884,814

DATE: 03/13/2002

TIME: 14:25:29

Input Set : A:\-11-1.app

Output Set: N:\CRF3\03132002\I884814.raw

3 <110> APPLICANT: Chen, Jin-Long  
 4 Amaral, M. Catherine  
 5 Tularik Inc.  
 7 <120> TITLE OF INVENTION: Human Uncoupling Protein 2 (hUCP2): Compositions and  
 8 Methods of Use  
 10 <130> FILE REFERENCE: 018781-001110US  
 12 <140> CURRENT APPLICATION NUMBER: US 09/884,814  
 13 <141> CURRENT FILING DATE: 2001-06-18  
 15 <150> PRIOR APPLICATION NUMBER: US 09/124,293  
 16 <151> PRIOR FILING DATE: 1998-07-29  
 18 <160> NUMBER OF SEQ ID NOS: 8  
 20 <170> SOFTWARE: PatentIn Ver. 2.1  
 22 <210> SEQ ID NO: 1  
 23 <211> LENGTH: 309  
 24 <212> TYPE: PRT  
 25 <213> ORGANISM: Homo sapiens  
 27 <220> FEATURE:  
 28 <223> OTHER INFORMATION: human uncoupling protein 2 (hUCP2) Chen (Tularik)  
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 34 20 25 30  
 35 Pro Leu Asp Thr Ala Lys Val Arg Leu Gln Ile Gln Gly Glu Ser Gln  
 36 35 40 45  
 37 Gly Pro Val Arg Ala Thr Ala Ser Ala Gln Tyr Arg Gly Val Met Gly  
 38 50 55 60  
 39 Thr Ile Leu Thr Met Val Arg Thr Glu Gly Pro Arg Ser Leu Tyr Asn  
 40 65 70 75 80  
 41 Gly Leu Val Ala Gly Leu Gln Arg Gln Met Ser Phe Ala Ser Val Arg  
 42 85 90 95  
 43 Ile Gly Leu Tyr Asp Ser Val Lys Gln Phe Tyr Thr Lys Gly Ser Glu  
 44 100 105 110  
 45 His Ala Ser Ile Gly Ser Arg Leu Leu Ala Gly Ser Thr Thr Gly Ala  
 46 115 120 125  
 47 Leu Ala Val Ala Val Ala Gln Pro Thr Asp Val Val Lys Val Arg Phe  
 48 130 135 140  
 49 Gln Ala Gln Ala Arg Ala Gly Gly Arg Arg Tyr Gln Ser Thr Val  
 50 145 150 155 160  
 51 Asn Ala Tyr Lys Thr Ile Ala Arg Glu Glu Gly Phe Arg Gly Leu Trp  
 52 165 170 175  
 53 Lys Gly Thr Ser Pro Asn Val Ala Arg Asn Ala Ile Val Asn Cys Ala  
 54 180 185 190

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55 Glu Leu Val Thr Tyr Asp Leu Ile Lys Asp Ala Leu Leu Lys Ala Asn  
 56 195 200 205  
 57 Leu Met Thr Asp Asp Leu Pro Cys His Phe Thr Ser Ala Phe Gly Ala  
 58 210 215 220  
 59 Gly Phe Cys Thr Thr Val Ile Ala Ser Pro Val Asp Val Val Lys Thr  
 60 225 230 235 240  
 61 Arg Tyr Met Asn Ser Ala Leu Gly Gln Tyr Ser Ser Ala Gly His Cys  
 62 245 250 255  
 63 Ala Leu Thr Met Leu Gln Lys Glu Gly Pro Arg Ala Phe Tyr Lys Gly  
 64 260 265 270  
 65 Phe Met Pro Ser Phe Leu Arg Leu Gly Ser Trp Asn Val Val Met Phe  
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 69 Arg Glu Ala Pro Phe  
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 75 <212> TYPE: DNA  
 76 <213> ORGANISM: Homo sapiens  
 78 <220> FEATURE:  
 79 <221> NAME/KEY: CDS  
 80 <222> LOCATION: (1)..(930)  
 81 <223> OTHER INFORMATION: human uncoupling protein 2 (hUCP2) Chen (Tularik)  
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 86 ttacagatcc aaggagaaag tcaggggcca gtgcgcgcta cagccagcgc ccagtaccgc 180  
 87 ggtgtatgg gcaccattct gaccatggtg cgtaactgagg gcccccaag cctctacaat 240  
 88 gggctgggtt ccggcctgca ggcggaaatg agcttgcct ctgtccgcatt cggcctgtat 300  
 89 gattctgtca aacagttcta caccaggcgt tctgagcatg ccagcattgg gagccgcctc 360  
 90 ctagcaggca gcaccacagg tgccctggct gtggctgtgg cccagccac ggatgtggta 420  
 91 aagggtccat tccaagctca ggcggggct ggaggtggtc ggagatacca aagcaccgtc 480  
 92 aatgcctaca agaccattgc ccgagaggaa gggttccggg gcctctggaa agggacctct 540  
 93 cccaatgtt ctcgtaatgc cattgtcaac tggctgtgg tggctgaccta tgacctcatc 600  
 94 aaggatgccc tcctgaaagc caacctcatg acagatgacc tcccttgcca cttcacttct 660  
 95 gcctttgggg caggcttctg caccatgtc atgcctccc ctgttagacgt ggtcaagacg 720  
 96 agatacatga actctgcctt gggccagtac agtagcgctg gccactgtgc ctttaccatg 780  
 97 ctccagaagg agggggccccc agccttctac aaagggttca tgccctcctt tctccgcttg 840  
 98 gtttccttggaa acgtgtatgg ttcgttacc tatgagcagc tgaaacgagc cctcatggct 900  
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 107 <220> FEATURE:  
 108 <223> OTHER INFORMATION: Description of Artificial Sequence:U1F primer  
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 111 atcaagctta tgggtgggtt caaggccaca gatg

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 PATENT APPLICATION: US/09/884,814 TIME: 14:25:29

Input Set : A:\-11-1.app  
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117 <213> ORGANISM: Artificial Sequence
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127 <211> LENGTH: 930
128 <212> TYPE: DNA
129 <213> ORGANISM: Homo sapiens
131 <220> FEATURE:
132 <221> NAME/KEY: CDS
133 <222> LOCATION: (1)..(930)
134 <223> OTHER INFORMATION: human uncoupling protein 2 (hUCP2) Tartaglia et al.
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141 ttt ctt ggg gct ggc aca gct gcc tgc atc gca gat ctc atc acc ttt 96
142 Phe Leu Gly Ala Gly Thr Ala Ala Cys Ile Ala Asp Leu Ile Thr Phe
143 20 25 30
145 cct ctg gat act gct aaa gtc cgg tta cag atc caa gga gaa agt cag 144
146 Pro Leu Asp Thr Ala Lys Val Arg Leu Gln Ile Gln Gly Glu Ser Gln
147 35 40 45
149 ggg cca gtg cgc gct aca gtc agc gcc cag tac cgc ggt gtg atg ggc 192
150 Gly Pro Val Arg Ala Thr Val Ser Ala Gln Tyr Arg Gly Val Met Gly
151 50 55 60
153 acc att ctg acc atg gtg cgt act gag ggc ccc cga agc ctc tac aat 240
154 Thr Ile Leu Thr Met Val Arg Thr Glu Gly Pro Arg Ser Leu Tyr Asn
155 65 70 75 80
157 ggg ctg gtt gcc ggc ctg cag cgc caa atg agc ttt gcc tct gtc cgc 288
158 Gly Leu Val Ala Gly Leu Gln Arg Gln Met Ser Phe Ala Ser Val Arg
159 85 90 95
161 atc ggc ctg tat gat tct gtc aaa cag ttc tac acc aag ggc tct gag 336
162 Ile Gly Leu Tyr Asp Ser Val Lys Gln Phe Tyr Thr Lys Gly Ser Glu
163 100 105 110
165 cat gcc agc att ggg agc cgc ctc cta gca ggc agc acc aca ggt gcc 384
166 His Ala Ser Ile Gly Ser Arg Leu Leu Ala Gly Ser Thr Thr Gly Ala
167 115 120 125
169 ctg gct gtg gct gtg gcc cag ccc acg gat gtg gta aag gtc cga ttc 432
170 Leu Ala Val Ala Val Ala Gln Pro Thr Asp Val Val Lys Val Arg Phe
171 130 135 140
173 caa gct cag gcc cgg gct gga ggt ggt cgg aga tac caa agc acc gtc 480
174 Gln Ala Gln Ala Arg Ala Gly Gly Arg Arg Tyr Gln Ser Thr Val
175 145 150 155 160
177 aat gcc tac aag acc att gcc cga gag gaa ggg ttc cgg ggc ctc tgg
178 Asn Ala Tyr Lys Thr Ile Ala Arg Glu Glu Phe Arg Gly Leu Trp
  
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179	165	170	175	
181	aaa ggg acc tct ccc aat gtt gct cgt aat gcc att gtc aac tgt gct			576
182	Lys Gly Thr Ser Pro Asn Val Ala Arg Asn Ala Ile Val Asn Cys Ala			
183	180	185	190	
185	gag ctg gtg acc tat gac ctc atc aag gat gcc ctc ctg aaa gcc aac			624
186	Glu Leu Val Thr Tyr Asp Leu Ile Lys Asp Ala Leu Leu Lys Ala Asn			
187	195	200	205	
189	ctc atg aca gat gac ctc cct tgc cac ttc act tct gcc ttt ggg gca			672
190	Leu Met Thr Asp Asp Leu Pro Cys His Phe Thr Ser Ala Phe Gly Ala			
191	210	215	220	
193	ggc ttc tgc acc act gtc atc gcc tcc cct gta gac gtg gtc aag acg			720
194	Gly Phe Cys Thr Thr Val Ile Ala Ser Pro Val Asp Val Val Lys Thr			
195	225	230	235	240
197	aga tac atg aac tct gcc ctg ggc cag tac agt agc gct ggc cac tgt			768
198	Arg Tyr Met Asn Ser Ala Leu Gly Gln Tyr Ser Ser Ala Gly His Cys			
199	245	250	255	
201	gcc ctt acc atg ctc cag aag gag ggg ccc cga gcc ttc tac aaa ggg			816
202	Ala Leu Thr Met Leu Gln Lys Glu Gly Pro Arg Ala Phe Tyr Lys Gly			
203	260	265	270	
205	ttc atg ccc tcc ttt ctc cgc ttg ggt tcc tgg aac gtg gtg atg ttc			864
206	Phe Met Pro Ser Phe Leu Arg Leu Gly Ser Trp Asn Val Val Met Phe			
207	275	280	285	
209	gtc acc tat gag cag ctg aaa cga gcc ctc atg gct gcc tgc act tcc			912
210	Val Thr Tyr Glu Gln Leu Lys Arg Ala Leu Met Ala Ala Cys Thr Ser			
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W-->	215 305	310		
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219	<211> LENGTH: 309			
220	<212> TYPE: PRT			
221	<213> ORGANISM: Homo sapiens			
223	<220> FEATURE:			
224	<223> OTHER INFORMATION: human uncoupling protein 2 (hUCP2) Tartaglia et al.			
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229	Phe Leu Gly Ala Gly Thr Ala Ala Cys Ile Ala Asp Leu Ile Thr Phe			
230	20	25	30	
231	Pro Leu Asp Thr Ala Lys Val Arg Leu Gln Ile Gln Gly Glu Ser Gln			
232	35	40	45	
233	Gly Pro Val Arg Ala Thr Val Ser Ala Gln Tyr Arg Gly Val Met Gly			
234	50	55	60	
235	Thr Ile Leu Thr Met Val Arg Thr Glu Gly Pro Arg Ser Leu Tyr Asn			
236	65	70	75	80
237	Gly Leu Val Ala Gly Leu Gln Arg Gln Met Ser Phe Ala Ser Val Arg			
238	85	90	95	
239	Ile Gly Leu Tyr Asp Ser Val Lys Gln Phe Tyr Thr Lys Gly Ser Glu			
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241 His Ala Ser Ile Gly Ser Arg Leu Leu Ala Gly Ser Thr Thr Gly Ala  
242 115 120 125  
243 Leu Ala Val Ala Val Ala Gln Pro Thr Asp Val Val Lys Val Arg Phe  
244 130 135 140  
245 Gln Ala Gln Ala Arg Ala Gly Gly Arg Arg Tyr Gln Ser Thr Val  
246 145 150 155 160  
247 Asn Ala Tyr Lys Thr Ile Ala Arg Glu Glu Gly Phe Arg Gly Leu Trp  
248 165 170 175  
249 Lys Gly Thr Ser Pro Asn Val Ala Arg Asn Ala Ile Val Asn Cys Ala  
250 180 185 190  
251 Glu Leu Val Thr Tyr Asp Leu Ile Lys Asp Ala Leu Leu Lys Ala Asn  
252 195 200 205  
253 Leu Met Thr Asp Asp Leu Pro Cys His Phe Thr Ser Ala Phe Gly Ala  
254 210 215 220  
255 Gly Phe Cys Thr Thr Val Ile Ala Ser Pro Val Asp Val Val Lys Thr  
256 225 230 235 240  
257 Arg Tyr Met Asn Ser Ala Leu Gly Gln Tyr Ser Ser Ala Gly His Cys  
258 245 250 255  
259 Ala Leu Thr Met Leu Gln Lys Glu Gly Pro Arg Ala Phe Tyr Lys Gly  
260 260 265 270  
261 Phe Met Pro Ser Phe Leu Arg Leu Gly Ser Trp Asn Val Val Met Phe  
262 275 280 285  
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265 Arg Glu Ala Pro Phe  
266 305  
269 <210> SEQ ID NO: 7  
270 <211> LENGTH: 930  
271 <212> TYPE: DNA  
272 <213> ORGANISM: Homo sapiens  
274 <220> FEATURE:  
275 <221> NAME/KEY: CDS  
276 <222> LOCATION: (1)..(930)  
277 <223> OTHER INFORMATION: human uncoupling protein 2 (hUCP2) Fleury et al.  
279 <400> SEQUENCE: 7  
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284 ttt ctt ggg gct ggc aca gct gcc tgc atc gca gat ctc atc acc ttt 96  
285 Phe Leu Gly Ala Gly Thr Ala Ala Cys Ile Ala Asp Leu Ile Thr Phe  
286 20 25 30  
288 cct ctg gat act gct aaa gtc cgg tta cag atc caa gga gaa agt cag 144  
289 Pro Leu Asp Thr Ala Lys Val Arg Leu Gln Ile Gln Gly Glu Ser Gln  
290 35 40 45  
292 ggg cca gtg cgc gct aca gcc agc gcc cag tac cgc ggt gtg atg ggc 192  
293 Gly Pro Val Arg Ala Thr Ala Ser Ala Gln Tyr Arg Gly Val Met Gly  
294 50 55 60  
296 acc att ctg acc atg gtg cgt act gag ggc ccc cga agc ctc tac aat 240  
297 Thr Ile Leu Thr Met Val Arg Thr Glu Gly Pro Arg Ser Leu Tyr Asn

**VERIFICATION SUMMARY**

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Input Set : A:\-11-1.app

Output Set: N:\CRF3\03132002\I884814.raw

L:215 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5

L:358 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:7